Evolutionary Biology Select

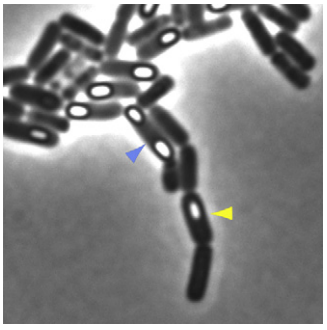
Cell

Life's ability to adapt to complex and changing environments is the subject of this issue's Evolutionary Biology Select. New findings suggest that microbes can prepare in advance for future changes in their environments and show that partial penetrance of a phenotype may be a stepping stone to dramatic evolutionary transitions. Other recent work links genetics and ecology, providing insight into the timing of flowering, disease susceptibility in nonhuman primates, and the impact of climate change on developmental plasticity in mammals.

Microbes Do More than Hedge Their Bets

It is often said that nothing endures but change. According to Mitchell et al. (2009), microorganisms have truly taken this lesson to heart. They provide surprising evidence that both the bacterium *Escherichia coli* and the budding yeast *Saccharomyces cerevisiae* have the capacity to prepare in advance for a change in their environment. The authors liken the phenomenon, termed adaptive prediction, to Pavlovian conditioning, in which an animal learns to associate the occurrence of one event with another, say a ringing bell and a food reward. In its life cycle in the intestinal track *E. coli* is exposed to the sugar lactose prior to exposure to maltose. The authors show that when a wild-type strain is exposed to lactose it leads to a partial upregulation of the genes responsive to maltose, but not vice versa. They then show that this wild-type strain has a selective advantage over a strain that has lost this capacity for adaptive prediction. The creation of the latter strain, which was evolved in the laboratory in just 500 generations in growth media lacking maltose and rich in lactose, points to just how readily adaptive prediction might be lost given an environment that does not favor its retention. The evolution of this strain also fits with the analogy to Pavlovian conditioning in that a conditioned response can be unlearned if the stimulus (in this case lactose) is repeatedly given but is not followed by the conditioned response (in this case maltose). The authors provide further support for the concept of adaptive prediction in an organism of greater complexity, *S. cerevisiae.* During the brewing process, yeast transition from fermentation to respiration. The various stresses associated with this process (such as low pH, heat, and oxidative stress) occur in a characteristic order. The authors examined whether pre-exposure to one stress improves survival of cells following exposure to a second stress. Only when the first stress precedes the second stress in the natural order does the pre-exposure confer appreciable cross-protection to the second stress. These findings have wide-reaching implications. Given that organisms outside of lab environments face cycles of environmental change, adaptive prediction may be a commonplace feature of life, one that will be understood only through the careful analysis of gene networks.
A. Mitchell et al. (2009). Nature ***460****, 220–224.*

Construction Noise



Sporulation signaling mutants in the bacterium *Bacillus subtilis* show multiple phenotypes, including the wild-type phenotype (single spore, yellow arrowhead) and a twin-sporulation phenotype (two spores, blue arrowhead). Image courtesy of A. Eldar.

When a mutation has an impact in some but not all organisms in a population, it is said to be partially penetrant. Although partial penetrance is usually attributed to genetic variation, it can also occur in genetically homogenous populations because of molecular fluctuations, or "noise." New findings by Eldar et al. (2009) show how partial penetrance of a phenotype may contribute to the evolution of new morphological traits. The authors studied the bacterium *Bacillus subtilis*, which form spores in response to nutrient limitation. During sporulation, *B. subtilis* cells divide into a forespore and a mother cell, and after formation of the septum, the two cells follow distinct developmental trajectories, with the forespore eventually becoming engulfed by the mother cell. The resulting spore then lies dormant in anticipation of a time with greater nutrient abundance. The authors studied mutants in which sporulation proceeds abnormally, at least in some cells, sometimes leading to cell death, instead of the generation of a viable spore, and in rare cases leading to the formation of two spores instead of one. The latter phenomenon is known as twin sporulation. In probing the factors that underlie this partial penetrance, the authors show that it is possible to systematically adjust the frequency of these different developmental fates by genetically manipulating chromosome replication and septation. In particular the authors show that it is possible to dramatically increase the frequency of twin sporulation and demonstrate that the mechanism of twin sporulation in these mutants resembles sporulation in the marine bacterium *Clostridium oceanicum* that natively forms twin spores. These findings suggest that partial penetrance could allow an organism to explore the potential adaptive advantages of a discrete morphological trait (in this case two spores instead of one) without having to commit to an irreversible all-or-nothing change.
A. Eldar et al. (2009). Nature. Published online July 5, 2009. 10.1038/nature08150.

Splicing Accounts for an Early Bloomer

Natural populations display phenotypic variations that may reflect adaptation to local environments. In recent work, Slotte et al. (2009) analyzed genes in the plant *Capsella bursa-pastoris* (commonly known as the Shepherd's Purse) in the search for polymorphisms that account for differences in flowering time. Studying plants originating from locations in Western Eurasia and China, they characterize changes in the splicing of the *FLOWERING LOCUS C (FLC)* as a potential

***Capsella bursa-pastoris* in flower. Image courtesy of T. Slotte.**

source for variation in flowering time in both populations. *FLC* was among the genes chosen for study because of its known role as a repressor of flowering in the model plant *Arabidopsis thaliana*. *C. bursa-pastoris* is tetraploid, and as a consequence there are duplicate paralogous copies of each gene (homeologs). The authors find two polymorphisms in the *FLC A* homeolog that affect splice sites and show that these correlate with early flowering. Interestingly, both polymorphisms result in the omission of exon 5 or in the absence of *FLC A* expression altogether. The authors highlight this discovery as an example of how loss-of-function mutations in a recently duplicated genome contribute to an adaptive phenotype. Future work may reveal additional types of mutations besides splicing that contribute to variation in tetraploid species of plants, which include many varieties of crops.
T. Slotte et al. (2009). Genetics. Published online July 6, 2009. 10.1534/genetics.109.103705.

Genetic Variation Gone Wild

Yellow baboons of the Amboseli basin of Kenya. Photo courtesy of J. Tung.

Although genetics and ecology are often confined to separate spheres of scientific study, the recent work by Tung et al. (2009) brings the two fields a step closer together. The authors provide evidence that a common genetic variant in yellow baboons confers a degree of resistance to infection by a malarial parasite. This is the first report linking a complex trait to a particular genotype in a wild population of nonhuman primates. The authors build on work in humans showing that a variant in the *cis*-regulatory region of the *FY* gene is protective against infection by the malarial parasite *Plasmodium vivax*. The *FY* gene encodes the receptor that *P. vivax* uses to gain entry into red blood cells. Tung et al. examined the *FY* locus in 190 wild yellow baboons and identified single-nucleotide polymorphisms (SNPs) in the gene's *cis*-regulatory region. They then show an association between an A/G polymorphism and the prevalence of infection by *Hepatocytsis*, a pathogen that has similarity to human malaria and afflicts baboons. The authors provide further evidence that the genotype of the *cis*-regulatory region influences the expression of the gene, both in vivo with an assessment of allelic imbalance and in vitro with the expression of a luciferase reporter linked to the variant *cis*-regulatory regions. Although the mechanism of protection is currently unclear, the study should inspire future efforts. Given the extensive ongoing study of primate behavior in the wild, these findings raise the possibility that it may one day be possible to link particular behavioral traits, such as aggression or sociability, to genetic factors.
J. Tung et al. (2009). Nature. Published online June 24, 2009. 10.1038/nature08149.

Ecological Downsizing

Developmental biologists working in the lab typically focus on genetic factors to understand variations in phenotypic traits such as body weight, but in natural environments an organism's development is subject to many different influences, such as competition and resource availability. Is it possible to assess the relative contributions of genes and the environment to phenotypic change in wild animals? Ozgul et al. (2009) tackle this question, and their answer clearly puts ecological factors in the driver's seat. Over the past two decades the wild Soay sheep of St. Kilda, an island off the far Northwest coast of Scotland, have been shrinking. The authors tease apart the reasons for this decline by analyzing the year by year changes in body weight and rates of survival and reproduction in the sheep population. Although an animal's weight is clearly influenced by heritable factors (the weight of the mother correlates with that of her offspring), the largest share of the variation in body weight is accounted for by changes in the environment. These findings suggest that an organism's ability to adapt its developmental program to suit environmental conditions may act as a buffer to limit the impact of selection.
A. Ozgul et al. (2009). Science. Published online July 2, 2009. 10.1126/science.1173668.

A Soay sheep (*Ovis aries*). Photo courtesy of A. Ozgul.

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